

JC17 Rec'd PCT/PTO 09 JUN 2005

## SEQUENCE LISTING

&lt;110&gt; Salonen, Jukka T

&lt;120&gt; Method for detecting a risk of hypertension and uses thereof

&lt;130&gt; Alpha-2B-AR variant

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 10

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 1344

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1341)

&lt;223&gt; Coding sequence for variant human alpha-2B-adrenoceptor protein

&lt;400&gt; 1

atg	gac	cac	cag	gac	ccc	tac	tcc	gtg	cag	gcc	aca	gcg	gcc	ata	gcg	48
Met	Asp	His	Gln	Asp	Pro	Tyr	Ser	Val	Gln	Ala	Thr	Ala	Ala	Ile	Ala	
1				5					10					15		

gcg	gcc	atc	acc	ttc	ctc	att	ctc	ttt	acc	atc	ttc	ggc	aac	gct	ctg	96
Ala	Ala	Ile	Thr	Phe	Leu	Ile	Leu	Phe	Thr	Ile	Phe	Gly	Asn	Ala	Leu	
			20					25					30			

gtc	atc	ctg	gct	gtg	ttg	acc	agc	cgc	tcg	ctg	cgc	gcc	cct	cag	aac	144
Val	Ile	Leu	Ala	Val	Leu	Thr	Ser	Arg	Ser	Leu	Arg	Ala	Pro	Gln	Asn	
			35				40					45				

ctg	ttc	ctg	gtg	tcg	ctg	gcc	gcc	gcc	gac	atc	ctg	gtg	gcc	acg	ctc	192
Leu	Phe	Leu	Val	Ser	Leu	Ala	Ala	Ala	Asp	Ile	Leu	Val	Ala	Thr	Leu	
			50				55					60				

atc	atc	cct	ttc	tcg	ctg	gcc	aac	gag	ctg	ctg	ggc	tac	tgg	tac	ttc	240
Ile	Ile	Pro	Phe	Ser	Leu	Ala	Asn	Glu	Leu	Leu	Gly	Tyr	Trp	Tyr	Phe	
					70					75					80	

cgg	cgc	acg	tgg	tgc	gag	gtg	tac	ctg	gcg	ctc	gac	gtg	ctc	ttc	tgc	288
Arg	Arg	Thr	Trp	Cys	Glu	Val	Tyr	Leu	Ala	Leu	Asp	Val	Leu	Phe	Cys	
				85					90					95		

acc	tcg	tcc	atc	gtg	cac	ctg	tgc	gcc	atc	agc	ctg	gac	cgc	tac	tgg	336
Thr	Ser	Ser	Ile	Val	His	Leu	Cys	Ala	Ile	Ser	Leu	Asp	Arg	Tyr	Trp	
			100					105					110			

gcc	gtg	agc	cgc	gcg	ctg	gag	tac	aac	tcc	aag	cgc	acc	ccg	cgc	cgc	384
Ala	Val	Ser	Arg	Ala	Leu	Glu	Tyr	Asn	Ser	Lys	Arg	Thr	Pro	Arg	Arg	
			115						120					125		

atc	aag	tgc	atc	atc	ctc	act	gtg	tgg	ctc	atc	gcc	gcc	gtc	atc	tcg	432
Ile	Lys	Cys	Ile	Ile	Leu	Thr	Val	Trp	Leu	Ile	Ala	Ala	Val	Ile	Ser	
			130				135						140			

ctg ccg ccc ctc atc tac aag ggc gac cag ggc ccc cag ccg cgc ggg	480
Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly	
145 150 155 160	
cgc ccc cag tgc aag ctc aac cag gag gcc tgg tac atc ctg gcc tcc	528
Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser	
165 170 175	
agc atc gga tct ttc ttt gct cct tgc ctc atc atg atc ctt gtc tac	576
Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr	
180 185 190	
ctg cgc atc tac ctg atc gcc aaa cgc agc aac cgc aga ggt ccc agg	624
Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg	
195 200 205	
gcc aag ggg ggg cct ggg cag ggt gag tcc aag cag ccc cga ccc gac	672
Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp	
210 215 220	
cat ggt ggg gct ttg gcc tca gcc aaa ctg cca gcc ctg gcc tct gtg	720
His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val	
225 230 235 240	
gct tct gcc aga gag gtc aac gga cac tcg aag tcc act ggg gag aag	768
Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys	
245 250 255	
gag gag ggg gag acc cct gaa gat act ggg acc cgg gcc ttg cca ccc	816
Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro	
260 265 270	
agt tgg gct gcc ctt ccc aac tca ggc cag ggc cag aag gag ggt gtt	864
Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val	
275 280 285	
tgt ggg gca tct cca gag gat gaa gct gaa gag gag gaa gag gag gag	912
Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu	
290 295 300	
gag gag tgt gaa ccc cag gca gtg cca gtg tct ccg gcc tca gct tgc	960
Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala Ser Ala Cys	
305 310 315 320	
agc ccc ccg ctg cag cag cca cag ggc tcc cgg gtg ctg gcc acc cta	1008
Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu Ala Thr Leu	
325 330 335	
cgt ggc cag gtg ctc ctg ggc agg ggc gtg ggt gct ata ggt ggg cag	1056
Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile Gly Gly Gln	
340 345 350	
tgg tgg cgt cga cgg gcg cag ctg acc cgg gag aag cgc ttc acc ttc	1104
Trp Trp Arg Arg Arg Ala Gln Leu Thr Arg Glu Lys Arg Phe Thr Phe	
355 360 365	
gtg ctg gct gtg gtc att ggc gtt ttt gtg ctc tgc tgg ttc ccc ttc	1152
Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe	
370 375 380	

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ttc ttc agc tac agc ctg ggc gcc atc tgc ccg aag cac tgc aag gtg 1200
Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His Cys Lys Val
385                390                395                400

ccc cat ggc ctc ttc cag ttc ttc ttc tgg atc ggc tac tgc aac agc 1248
Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser
                405                410                415

tca ctg aac cct gtt atc tac acc atc ttc aac cag gac ttc cgc cgt 1296
Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg
                420                425                430

gcc ttc cgg agg atc ctg tgc cgc ccg tgg acc cag acg gcc tgg tga 1344
Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr Ala Trp
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<210> 2
<211> 447
<212> PRT
<213> Homo sapiens

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Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
                20                25                30

Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
                35                40                45

Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
                50                55                60

Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
                65                70                75                80

Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
                85                90                95

Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
                100                105                110

Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
                115                120                125

Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
                130                135                140

Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
                145                150                155                160

Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
                165                170                175

Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
                180                185                190

Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
                195                200                205

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Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp  
 210 215 220  
 His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val  
 225 230 235 240  
 Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys  
 245 250 255  
 Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro  
 260 265 270  
 Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val  
 275 280 285  
 Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu  
 290 295 300  
 Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala Ser Ala Cys  
 305 310 315 320  
 Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu Ala Thr Leu  
 325 330 335  
 Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile Gly Gly Gln  
 340 345 350  
 Trp Trp Arg Arg Arg Ala Gln Leu Thr Arg Glu Lys Arg Phe Thr Phe  
 355 360 365  
 Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe  
 370 375 380  
 Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His Cys Lys Val  
 385 390 395 400  
 Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser  
 405 410 415  
 Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg  
 420 425 430  
 Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr Ala Trp  
 435 440 445

&lt;210&gt; 3

&lt;211&gt; 1353

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1350)

&lt;223&gt; Coding sequence for human alpha-2B-adrenoceptor protein

&lt;400&gt; 3

atg gac cac cag gac ccc tac tcc gtg cag gcc aca gcg gcc ata gcg  
 Met Asp His Gln Asp Pro Tyr Ser Val Gln Ala Thr Ala Ala Ile Ala  
 1 5 10 15

48

gcg gcc atc acc ttc ctc att ctc ttt acc atc ttc ggc aac gct ctg Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu 20 25 30	96
gtc atc ctg gct gtg ttg acc agc cgc tcg ctg cgc gcc cct cag aac Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn 35 40 45	144
ctg ttc ctg gtg tcg ctg gcc gcc gcc gac atc ctg gtg gcc acg ctc Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu 50 55 60	192
atc atc cct ttc tcg ctg gcc aac gag ctg ctg ggc tac tgg tac ttc Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe 65 70 75 80	240
cgg cgc acg tgg tgc gag gtg tac ctg gcg ctc gac gtg ctc ttc tgc Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys 85 90 95	288
acc tcg tcc atc gtg cac ctg tgc gcc atc agc ctg gac cgc tac tgg Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp 100 105 110	336
gcc gtg agc cgc gcg ctg gag tac aac tcc aag cgc acc ccg cgc cgc Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg 115 120 125	384
atc aag tgc atc atc ctc act gtg tgg ctc atc gcc gcc gtc atc tcg Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser 130 135 140	432
ctg ccg ccc ctc atc tac aag ggc gac cag ggc ccc cag ccg cgc ggg Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly 145 150 155 160	480
cgc ccc cag tgc aag ctc aac cag gag gcc tgg tac atc ctg gcc tcc Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser 165 170 175	528
agc atc gga tct ttc ttt gct cct tgc ctc atc atg atc ctt gtc tac Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr 180 185 190	576
ctg cgc atc tac ctg atc gcc aaa cgc agc aac cgc aga ggt ccc agg Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg 195 200 205	624
gcc aag ggg ggg cct ggg cag ggt gag tcc aag cag ccc cga ccc gac Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp 210 215 220	672
cat ggt ggg gct ttg gcc tca gcc aaa ctg cca gcc ctg gcc tct gtg His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val 225 230 235 240	720

gct tct gcc aga gag gtc aac gga cac tcg aag tcc act ggg gag aag	768
Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys	
245 250 255	
gag gag ggg gag acc cct gaa gat act ggg acc cgg gcc ttg cca ccc	816
Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro	
260 265 270	
agt tgg gct gcc ctt ccc aac tca ggc cag ggc cag aag gag ggt gtt	864
Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val	
275 280 285	
tgt ggg gca tct cca gag gat gaa gct gaa gag gag gaa gag gag gag	912
Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu	
290 295 300	
gag gag gag gaa gag tgt gaa ccc cag gca gtg cca gtg tct ccg gcc	960
Glu Glu Glu Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala	
305 310 315 320	
tca gct tgc agc ccc ccg ctg cag cag cca cag ggc tcc cgg gtg ctg	1008
Ser Ala Cys Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu	
325 330 335	
gcc acc cta cgt ggc cag gtg ctc ctg ggc agg ggc gtg ggt gct ata	1056
Ala Thr Leu Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile	
340 345 350	
ggt ggg cag tgg tgg cgt cga cgg gcg cag ctg acc cgg gag aag cgc	1104
Gly Gly Gln Trp Trp Arg Arg Ala Gln Leu Thr Arg Glu Lys Arg	
355 360 365	
ttc acc ttc gtg ctg gct gtg gtc att ggc gtt ttt gtg ctc tgc tgg	1152
Phe Thr Phe Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp	
370 375 380	
ttc ccc ttc ttc ttc agc tac agc ctg ggc gcc atc tgc ccg aag cac	1200
Phe Pro Phe Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His	
385 390 395 400	
tgc aag gtg ccc cat ggc ctc ttc cag ttc ttc ttc tgg atc ggc tac	1248
Cys Lys Val Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr	
405 410 415	
tgc aac agc tca ctg aac cct gtt atc tac acc atc ttc aac cag gac	1296
Cys Asn Ser Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp	
420 425 430	
ttc cgc cgt gcc ttc cgg agg atc ctg tgc cgc ccg tgg acc cag acg	1344
Phe Arg Arg Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr	
435 440 445	
gcc tgg tga	1353
Ala Trp	
450	

&lt;210&gt; 4

&lt;211&gt; 450

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 4

Met Asp His Gln Asp Pro Tyr Ser Val Gln Ala Thr Ala Ala Ile Ala  
1 5 10 15

Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu  
20 25 30

Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn  
35 40 45

Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu  
50 55 60

Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe  
65 70 75 80

Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys  
85 90 95

Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp  
100 105 110

Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg  
115 120 125

Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser  
130 135 140

Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly  
145 150 155 160

Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser  
165 170 175

Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr  
180 185 190

Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg  
195 200 205

Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp  
210 215 220

His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val  
225 230 235 240

Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys  
245 250 255

Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro  
260 265 270

Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val  
275 280 285

Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu  
290 295 300

Glu Glu Glu Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala  
305 310 315 320

Ser Ala Cys Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu  
 325 330 335  
 Ala Thr Leu Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile  
 340 345 350  
 Gly Gly Gln Trp Trp Arg Arg Arg Ala Gln Leu Thr Arg Glu Lys Arg  
 355 360 365  
 Phe Thr Phe Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp  
 370 375 380  
 Phe Pro Phe Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His  
 385 390 395 400  
 Cys Lys Val Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr  
 405 410 415  
 Cys Asn Ser Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp  
 420 425 430  
 Phe Arg Arg Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr  
 435 440 445  
 Ala Trp  
 450

<210> 5  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer pair

<400> 5  
 ggggcgaacgc tcttgtcta

19

<210> 6  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer pair

<400> 6  
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19

<210> 7  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer pair

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 gcagcaaccg cagaggtc

18



<210> 8  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer pair

<400> 8  
gggcaagaag cagggtgac 19

<210> 9  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer pair

<400> 9  
agggtgtttg tggggcatct 20

<210> 10  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer pair

<400> 10  
caagctgagg ccggagacac t 21